



Sequence Listing

<110> Chou, Min-Yuan
Leu, Charng-Yih

<120> Novel Human alpha 1 Chain Collagen

<130> 32350-176844

<140> US 09/996,611

<141> 2001-11-30

<150> TAIWAN 89128027

<151> 2000-12-27

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<212> PRT

<213> Homo sapiens

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<223> alpha 1 chain collagen
Pro in this sequence stands for hydroxyproline

<400> 1

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Cys	Arg	Thr	Ala	Pro	Thr	Asp	Leu	Val	Phe	Ile	Leu	Asp	Gly	Ser
				35					40					45
Tyr	Ser	Val	Gly	Pro	Glu	Asn	Phe	Glu	Ile	Val	Lys	Lys	Trp	Leu
				50					55					60
Val	Asn	Ile	Thr	Lys	Asn	Phe	Asp	Ile	Gly	Pro	Lys	Phe	Ile	Gln
				65					70					75
Val	Gly	Val	Val	Gln	Tyr	Ser	Asp	Tyr	Pro	Val	Leu	Glu	Ile	Pro
				80					85					90
Leu	Gly	Ser	Tyr	Asp	Ser	Gly	Glu	His	Leu	Thr	Ala	Ala	Val	Glu
				95					100					105
Ser	Ile	Leu	Tyr	Leu	Gly	Gly	Asn	Thr	Lys	Thr	Gly	Lys	Ala	Ile
				110					115					120

Gln	Phe	Ala	Leu	Asp	Tyr	Leu	Phe	Ala	Lys	Ser	Ser	Arg	Phe	Leu	125	130	135
Thr	Lys	Ile	Ala	Val	Val	Leu	Thr	Asp	Gly	Lys	Ser	Gln	Asp	Asp	140	145	150
Val	Lys	Asp	Ala	Ala	Gln	Ala	Ala	Arg	Asp	Ser	Lys	Ile	Thr	Leu	155	160	165
Phe	Ala	Ile	Gly	Val	Gly	Ser	Glu	Thr	Glu	Asp	Ala	Glu	Leu	Arg	170	175	180
Ala	Ile	Ala	Asn	Lys	Pro	Ser	Ser	Thr	Tyr	Val	Phe	Tyr	Val	Glu	185	190	195
Asp	Tyr	Ile	Ala	Ile	Ser	Lys	Ile	Arg	Glu	Val	Met	Lys	Gln	Lys	200	205	210
Leu	Cys	Glu	Glu	Ser	Val	Cys	Pro	Thr	Arg	Ile	Pro	Val	Ala	Ala	215	220	225
Arg	Asp	Glu	Arg	Gly	Phe	Asp	Ile	Leu	Leu	Gly	Leu	Asp	Val	Asn	230	235	240
Lys	Lys	Val	Lys	Lys	Arg	Ile	Gln	Leu	Ser	Pro	Lys	Lys	Ile	Lys	245	250	255
Gly	Tyr	Glu	Val	Thr	Ser	Lys	Val	Asp	Leu	Ser	Glu	Leu	Thr	Ser	260	265	270
Asn	Val	Phe	Pro	Glu	Gly	Leu	Pro	Pro	Ser	Tyr	Val	Phe	Val	Ser	275	280	285
Thr	Gln	Arg	Phe	Lys	Val	Lys	Lys	Ile	Trp	Asp	Leu	Trp	Arg	Ile	290	295	300
Leu	Thr	Ile	Asp	Gly	Arg	Pro	Gln	Ile	Ala	Val	Thr	Leu	Asn	Gly	305	310	315
Val	Asp	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Thr	Ser	Val	Ile	Asn	Gly	320	325	330
Ser	Gln	Val	Val	Thr	Phe	Ala	Asn	Pro	Gln	Val	Lys	Thr	Leu	Phe	335	340	345
Asp	Glu	Gly	Trp	His	Gln	Ile	Arg	Leu	Leu	Val	Thr	Glu	Gln	Asp	350	355	360
Val	Thr	Leu	Tyr	Ile	Asp	Asp	Gln	Gln	Ile	Glu	Asn	Lys	Pro	Leu	365	370	375

His	Pro	Val	Leu	Gly	Ile	Leu	Ile	Asn	Gly	Gln	Thr	Gln	Ile	Gly	380	385	390
Lys	Tyr	Ser	Gly	Lys	Glu	Glu	Thr	Val	Gln	Phe	Asp	Val	Gln	Lys	395	400	405
Leu	Arg	Ile	Tyr	Cys	Asp	Pro	Glu	Gln	Asn	Asn	Arg	Glu	Thr	Ala	410	415	420
Cys	Glu	Ile	Pro	Gly	Phe	Cys	Leu	Asn	Gly	Pro	Ser	Asp	Val	Gly	425	430	435
Ser	Thr	Pro	Ala	Pro	Cys	Ile	Cys	Pro	Pro	Gly	Lys	Pro	Gly	Leu	440	445	450
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Ala	Gly	Thr	Pro	Gly	Val	Pro	Gly	Ser	Pro	Gly	Ile	Gln	Gly	Ala	485	490	495
Arg	Gly	Leu	Pro	Gly	Tyr	Lys	Gly	Glu	Pro	Gly	Arg	Asp	Gly	Asp	500	505	510
Lys	Gly	Asp	Arg	Gly	Leu	Pro	Gly	Phe	Pro	Gly	Leu	His	Gly	Met	515	520	525
Pro	Gly	Ser	Lys	Gly	Glu	Met	Gly	Ala	Lys	Gly	Asp	Lys	Gly	Ser	530	535	540
Pro	Gly	Phe	Tyr	Gly	Lys	Lys	Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asn	545	550	555
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His	Gly	Lys	Asp	Gly	Leu	Met	Gly	Ser	Pro	Gly	Phe	Lys	Gly	Glu	575	580	585
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Pro	Gly	Ile	Pro	Gly	Phe	Pro	Gly	Asn	Arg	Gly	Leu	Met	Gly	Gln	605	610	615
Lys	Gly	Glu	Ile	Gly	Pro	Pro	Gly	Gln	Gln	Gly	Lys	Lys	Gly	Ala	620	625	630
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Thr	Gly	Ser	Pro	Gly 680	Glu	Pro	Gly	Tyr	Met	Gly	Leu	Pro	Gly	Ile 690
Gln	Gly	Lys	Lys	Gly 695	Asp	Lys	Gly	Asn	Gln	Gly	Glu	Lys	Gly	Ile 705
Gln	Gly	Gln	Lys	Gly 710	Glu	Asn	Gly	Arg	Gln	Gly	Ile	Pro	Gly	Gln 720
Gln	Gly	Ile	Gln	Gly 725	His	His	Gly	Ala	Lys	Gly	Glu	Arg	Gly	Glu 735
Lys	Gly	Glu	Pro	Gly 740	Val	Arg	Gly	Ala	Ile	Gly	Ser	Lys	Gly	Glu 750
Ser	Gly	Val	Asp	Gly 755	Leu	Met	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Gln 765
Pro	Gly	Asp	Pro	Gly 770	Pro	Gln	Gly	Pro	Pro	Gly	Leu	Asp	Gly	Lys 780
Pro	Gly	Arg	Glu	Phe 785	Ser	Glu	Gln	Phe	Ile	Arg	Gln	Val	Cys	Thr 795
Asp	Val	Ile	Arg	Ala 800	Gln	Leu	Pro	Val	Leu	Leu	Gln	Ser	Gly	Arg 810
Ile	Arg	Asn	Cys	Asp 815	His	Cys	Leu	Ser	Gln	His	Gly	Ser	Pro	Gly 825
Ile	Pro	Gly	Pro	Pro 830	Gly	Pro	Ile	Gly	Pro	Glu	Gly	Pro	Arg	Gly 840
Leu	Pro	Gly	Leu	Pro 845	Gly	Arg	Asp	Gly	Val	Pro	Gly	Leu	Val	Gly 855
Val	Pro	Gly	Arg	Pro 860	Gly	Val	Arg	Gly	Leu	Lys	Gly	Leu	Pro	Gly 870
Arg	Asn	Gly	Glu	Lys 875	Gly	Ser	Gln	Gly	Phe	Gly	Tyr	Pro	Gly	Glu 885
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Ser	Lys	Glu	Gly	Pro	Pro	Gly	Asp	Pro	Gly	Leu	Pro	Gly	Lys	Asp
				905					910					915

Gly	Asp	His	Gly	Lys	Pro	Gly	Ile	Gln	Gly	Gln	Pro	Gly	Pro	Pro
				920					925					930

Gly	Ile	Cys	Asp	Pro	Ser	Leu	Cys	Phe	Ser	Val	Ile	Ala	Arg	Arg
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Asp	Leu	Val	Phe	Ile	Leu	Asp	Gly	Ser	Tyr	Ser	Val	Gly	Pro	Glu
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				20					25					30

Phe	Asp	Ile	Gly	Pro	Lys	Phe	Ile	Gln	Val	Gly	Val	Val	Gln	Tyr
				35					40					45

Ser	Asp	Tyr	Pro	Val	Leu	Glu	Ile	Pro	Leu	Gly	Ser	Tyr	Asp	Ser
				50					55					60

Gly	Glu	His	Leu	Thr	Ala	Ala	Val	Glu	Ser	Ile	Leu	Tyr	Leu	Gly
				65					70					75

Gly	Asn	Thr	Lys	Thr	Gly	Lys	Ala	Ile	Gln	Phe	Ala	Leu	Asp	Tyr
				80					85					90

Leu	Phe	Ala	Lys	Ser	Ser	Arg	Phe	Leu	Thr	Lys	Ile	Ala	Val	Val
				95					100					105

Leu	Thr	Asp	Gly	Lys	Ser	Gln	Asp	Asp	Val	Lys	Asp	Ala	Ala	Gln
				110					115					120

Ala	Ala	Arg	Asp	Ser	Lys	Ile	Thr	Leu	Phe	Ala	Ile	Gly	Val	Gly
				125					130					135

Ser	Glu	Thr	Glu	Asp	Ala	Glu	Leu	Arg	Ala	Ile	Ala	Asn	Lys	Pro
				140					145					150

Ser	Ser	Thr	Tyr	Val	Phe	Tyr	Val	Glu	Asp	Tyr	Ile	Ala	Ile	Ser
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Lys	Ile	Arg	Glu	Val	Met
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<211> 183

<212> PRT

<213> Homo sapiens

<220>

<223> Thrombospondin N-terminal-like domain

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				20					25					30

Thr	Ser	Lys	Val	Asp	Leu	Ser	Glu	Leu	Thr	Ser	Asn	Val	Phe	Pro
				35					40					45

Glu	Gly	Leu	Pro	Pro	Ser	Tyr	Val	Phe	Val	Ser	Thr	Gln	Arg	Phe
				50					55					60

Lys	Val	Lys	Lys	Ile	Trp	Asp	Leu	Trp	Arg	Ile	Leu	Thr	Ile	Asp
				65					70					75

Gly	Arg	Pro	Gln	Ile	Ala	Val	Thr	Leu	Asn	Gly	Val	Asp	Lys	Ile
				80					85					90

Leu	Leu	Phe	Thr	Thr	Thr	Ser	Val	Ile	Asn	Gly	Ser	Gln	Val	Val
				95					100					105

Thr	Phe	Ala	Asn	Pro	Gln	Val	Lys	Thr	Leu	Phe	Asp	Glu	Gly	Trp
				110					115					120

His	Gln	Ile	Arg	Leu	Leu	Val	Thr	Glu	Gln	Asp	Val	Thr	Leu	Tyr
				125					130					135

Ile	Asp	Asp	Gln	Gln	Ile	Glu	Asn	Lys	Pro	Leu	His	Pro	Val	Leu
				140					145					150

Gly	Ile	Leu	Ile	Asn	Gly	Gln	Thr	Gln	Ile	Gly	Lys	Tyr	Ser	Gly
				155					160					165

Lys	Glu	Glu	Thr	Val	Gln	Phe	Asp	Val	Gln	Lys	Leu	Arg	Ile	Tyr
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Cys Asp Pro

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<213> Homo sapiens

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Pro in this sequence stands for hydroxyproline

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Gly	Asn	Pro	Gly	Tyr	Pro	Gly	Gln	Pro	Gly	Gln	Asp	Gly	Lys	Pro
				20					25					30
Gly	Tyr	Gln	Gly	Ile	Ala	Gly	Thr	Pro	Gly	Val	Pro	Gly	Ser	Pro
				35					40					45
Gly	Ile	Gln	Gly	Ala	Arg	Gly	Leu	Pro	Gly	Tyr	Lys	Gly	Glu	Pro
				50					55					60
Gly	Arg	Asp	Gly	Asp	Lys	Gly	Asp	Arg	Gly	Leu	Pro	Gly	Phe	Pro
				65					70					75
Gly	Leu	His	Gly	Met	Pro	Gly	Ser	Lys	Gly	Glu	Met	Gly	Ala	Lys
				80					85					90
Gly	Asp	Lys	Gly	Ser	Pro	Gly	Phe	Tyr	Gly	Lys	Lys	Gly	Ala	Lys
				95					100					105
Gly	Glu	Lys	Gly	Asn	Ala	Gly	Phe	Pro	Gly	Leu	Pro	Gly	Pro	Ala
				110					115					120
Gly	Glu	Pro	Gly	Arg	His	Gly	Lys	Asp	Gly	Leu	Met	Gly	Ser	Pro
				125					130					135
Gly	Phe	Lys	Gly	Glu	Ala	Gly	Ser	Pro	Gly	Ala	Pro	Gly	Gln	Asp
				140					145					150
Gly	Thr	Arg	Gly	Glu	Pro	Gly	Ile	Pro	Gly	Phe	Pro	Gly	Asn	Arg
				155					160					165
Gly	Leu	Met	Gly	Gln	Lys	Gly	Glu	Ile	Gly	Pro	Pro	Gly	Gln	Gln
				170					175					180
Gly	Lys	Lys	Gly	Ala	Pro	Gly	Met	Pro	Gly	Leu	Met	Gly	Ser	Asn
				185					190					195

Gly Ser Pro Gly	Gln Pro Gly Thr Pro	Gly Ser Lys Gly Ser Lys	200	205	210
Gly Glu Pro Gly	Ile Gln Gly Met Pro	Gly Ala Ser Gly Leu Lys	215	220	225
Gly Glu Pro Gly	Ala Thr Gly Ser Pro	Gly Glu Pro Gly Tyr Met	230	235	240
Gly Leu Pro Gly	Ile Gln Gly Lys Lys	Gly Asp Lys Gly Asn Gln	245	250	255
Gly Glu Lys Gly	Ile Gln Gly Gln Lys	Gly Glu Asn Gly Arg Gln	260	265	270
Gly Ile Pro Gly	Gln Gln Gly Ile Gln	Gly His His Gly Ala Lys	275	280	285
Gly Glu Arg Gly	Glu Lys Gly Glu Pro	Gly Val Arg Gly Ala Ile	290	295	300
Gly Ser Lys Gly	Glu Ser Gly Val Asp	Gly Leu Met Gly Pro Ala	305	310	315
Gly Pro Lys Gly	Gln Pro Gly Asp Pro	Gly Pro Gln Gly Pro Pro	320	325	330
Gly Leu Asp Gly	Lys Pro Gly Arg Glu	Phe Ser Glu Gln Phe Ile	335	340	345
Arg Gln Val Cys	Thr Asp Val Ile Arg	Ala Gln Leu Pro Val Leu	350	355	360
Leu Gln Ser Gly	Arg Ile Arg Asn Cys	Asp His Cys Leu Ser Gln	365	370	375
His Gly Ser Pro	Gly Ile Pro Gly Pro	Pro Gly Pro Ile Gly Pro	380	385	390
Glu Gly Pro Arg	Gly Leu Pro Gly Leu	Pro Gly Arg Asp Gly Val	395	400	405
Pro Gly Leu Val	Gly Val Pro Gly Arg	Pro Gly Val Arg Gly Leu	410	415	420
Lys Gly Leu Pro	Gly Arg Asn Gly Glu	Lys Gly Ser Gln Gly Phe	425	430	435
Gly Tyr Pro Gly	Glu Gln Gly Pro Pro	Gly Pro Pro Gly Pro Glu	440	445	450

Gly	Pro	Pro	Gly	Ile	Ser	Lys	Glu	Gly	Pro	Pro	Gly	Asp	Pro	Gly
				455					460					465
Leu	Pro	Gly	Lys	Asp	Gly	Asp	His	Gly	Lys	Pro	Gly	Ile	Gln	Gly
				470					475					480
Gln	Pro	Gly	Pro	Pro	Gly	Ile	Cys	Asp	Pro	Ser	Leu	Cys	Phe	Ser
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Val	Ile	Ala	Arg	Arg	Asp	Pro	Phe	Arg	Lys	Gly	Pro	Asn	Tyr	
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**SEQUENCE LISTING**

SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 954 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(iii) FEATURE:

(A) NAME: Alpha 1 chain collagen

10 (B) OTHER INFORMATION: /note="Where
P=P*=Hydroxyproline"

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15	TAAVESILYLGGNTKTGKAIQFALDYLFAKSSRFLT KIAVVLTDGKSQDD	150
	VKDAAQAARDSKITLFAIGVGSETEDAE LRAIANKPSSTYVFYVEDYIAI	200
	SKIREVMKQKLCEESVCPTRIPVAARDERGF DILLGLDVNKKVKKRIQLS	250
	PKKIKGYEVT SKVDLSELTSNVFPEGLPPSYV FVSTQRFKVKKIWDLWRI	300
	LTIDGRPQIAVTLNGVDKILLFTTT SVINGSQVVTFANPQVKTLFDEGWH	350
20	QIRLLVTEQDVTLYIDDQQIENKPLHPVLGILINGQTQIGKYSGKEETVQ	400
	FDVQKLRIYCDPEQNNRETACEIPGFCLNGPSDVGSTPAPCICPPGKPGL	450
	QGPKGDPGLPGNPGYPGQPGQDGKPGYQGIAGTPGVPGSPGIQGARGLP	500
	YKGEPGRDGDGKDRGLPGFPGLHGMPSK GEMGAKGDKGSPGFYGKKGAK	550
	GEKGNAGFPGLPGPAGEPGRHKG DGLMGSPGFKGEAGSPGAPGQDGTRGE	600
25	PGIPGFPGNRGLMGQKGEIGPPGQQGKKGAPGMPGLMGSNGSPGQPGTPG	650
	SKGSKGEPGIQGMPGASGLKGE PGATGSPGEPGYMGLPGIQGKKGDKNQ	700
	GEKGIQGQKGENRQGI PGQQGIQGHGAKGERGEKGE PGVRGAIGSKGE	750
	SGVDGLMPAGPKGQPGDPGPQGPGLDGKPGREFSEQFIRQVCTDVIRA	800
	QLPVLLQSGRIRNCDHCLSQHGS PGIPGPPGPIGPEGPRGLPGLPGRDGV	850
30	PGLVGVPPRPGVRGLKGLPGRNGE KGSQGFYGPGEQGP PGPPGPEGPPGI	900
	SKEGPPGDPGLPGKGDH GKPGIQGP GPPGICDPSLCFSVIARRDPFRK	950
	GPNY 954	

SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(iii) FEATURE:

(A) NAME: von Willebrand factor A domain

10

DLVFILDGSSVGPENFEIVKKWLVNITKNFDIGPKFIQVGVVQYSDYPV	50
LEIPLGSYDSGEHLTAAVESILYLGNTKTGKAIQFALDYLFKSSRFLT	100
KIAVVLTDGKSQDDVKDAAQAARDSKITLFAIGVGSETEDAELRAIANKP	150
SSTYVFYVEDYIAISKIREVM	171

15

SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(iii) FEATURE:

(A) NAME: Thrombospondin N-terminal-like domain

25

GFDILLGLDVNKKVKKRIQLSPKKIKGYEVTSKVDLSELTSNVFPEGLPP	50
SYVVFVSTQRFKVKKIWDLWRILTIDGRPQIAVTLNGVDKILLFTTTSVIN	100
GSQVVTFANPQVKTLFDEGWHQIRLLVTEQDVTLYIDDQQIENKPLHPVL	150
GILINGQTQIGKYSKKEETVQFDVQKLRIYCDP	183

30

SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

5 (iii) FEATURE:

(C) NAME: collagenous domain

(D) OTHER INFORMATION: /note="Where
P=P*=Hydroxyproline"

10

	GKPGQLQGPKGDPGLPGNPGYPGQPGQDGKPGYQGIAGTPGVPGSPGIQGA	50
	RGLPGYKGEPGRDGDGKDRGLPGFPGLHGMPSKGEAKGDKGSPGFYG	100
	KKGAKGEKGNAGFPGLPGPAGEPGRHGKDGLMGSPGFKGEAGSPGAPGQD	150
15	GTRGEPGIPGFPGNRGLMGQKGEIGPPGQQGKKGAPGMPGLMGSNGSPGQ	200
	PGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGYMGLPGIQGKKG	250
	DKGNQGEKGIQGQKGENGRQGI PGQQGIQGHGAKGERGEKGEPEGVRGAI	300
	GSKGESGVDGLMPAGPKGQPGDPGPQGPPGLDGKPGREFSEQFIRQVCT	350
	DVIRAQLPVLLQSGRIRNCDHCLSQHGSPIPGPPGPIGPEGPRGLPGLP	400
20	GRDGVPLVGVPGRPGVRGLKGLPGRNGEKGSQGFYYPGEQPPGPPGPE	450
	GPPGISKEGPPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARR	500
	DPFRKGPNY 509	

25 SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2865 base pairs

(B) TYPE: nucleic acid

(iv) MOLECULE TYPE: cDNA

30 (v) FEATURE: Alpha 1 chain collagen

	atggctcactatattacatttctctgcatggtttgggtgctgcttcttcagaattctgtg	60
	ttagctgaagatggggaagtaagatcaagttgtcgtactgctccgacagatttagtttct	120
	atcttagatggctctttagtggtggcccagaaaactttgaaatagtgaaaaagtggtt	180
	gtcaatatcacaaaaaactttgacatagggccgaagtttattcaagttggagtgggtcaa	240
5	tatagtgactaccctgtgctggagattcctctcggaagctatgattcaggagaacatttg	300
	acggcagcagtggaatccatactctacttaggaggaaacacaaagacagggaaggccatc	360
	cagtttgcgctcgattacctttttgccaagtcctcacgatttctgactaagatagcagt	420
	gtacttacggatggcaaattccaagatgacgtcaaggatgcagctcaagcagcaagagat	480
	agtaagataacattatttgctattggtgttggttcagaaacagaagatgccgaacttaga	540
10	gctattgccaacaagccttcgtctacttatgtgttttatgtggaagactatattgcaata	600
	tccaaaataagggaagtgtgaagcagaaactttgtgaagaatctgtctgtccaacacga	660
	attccagtggtcagctcgtgatgaaaggggatttgatattcttttaggttagatgtaaat	720
	aaaaagggttaagaaaagaatacagctttcacaaaaaagataaaaaggatatgaagtaaca	780
	tcaaaagttgatttatcagaactcacaaagcaatgttttccagaagggtcttctccatca	840
15	tatgtatttggtgtctactcaaagatttaaagtcaagaaaatttgggatttatggagaata	900
	ttaactattgatggaaggccacaaatagcagttaccttaaagtgtggacaaaatctta	960
	ttatttacaacaaccagcgtaattaatggctcacaagtgggtacctttgctaaccctcaa	1020
	gttaagacgttggttgatgaaggctggcaccaaattcgtctcttagtaacagaacaagat	1080
	gtgactttgtatattgatgaccaacaaattgaaaacaagcccttacatccagttttagg	1140
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	tttgatgtccaaaagttgcgaatctactgtgaccagaacagaacaaccgggagacagca	1260
	tgtgagattcctggattttgccttaatgggtcccagtgatgtagggtcaactccagctccc	1320
	tgtatttgctctccgggaaaaccaggacttcaaggcccaaagggtgacctggactgcct	1380
	gggaaccctggctaccctggacaacctgggtcaagatggtaagcctggatatcagggaatt	1440
25	gcaggagaccaggtgttcaggatctccaggaatacaaggagctcgaggactaccaggt	1500
	tacaaaggagaaccagggcgagatgggtgacaagggtgatcgtggacttcttggttttct	1560
	gggcttcatggcatgccaggatcaaagggtgaaatgggtgccaaaggagacaaaggatca	1620
	cctggattttatggcaaaaagggtgcaaaagggtgaaaaggggaatgctggcttccctggc	1680
	ctccctggacctgctggagaaccaggaagacatggaaaggatggattaatgggtagtccc	1740
30	ggtttcaaggggagaagcaggatcccctgggtgctccggggcaggatggaacacggggagag	1800
	cctggaatcccaggatttcttggaaccgaggattaatgggcccaggagaaattggg	1860
	cctccaggacagcaaggaaaaaaaggagccccagggtgctgtttaaagggaagcaat	1920
	ggctcaccaggccagcctggaacaccgggatctaagggaagcaaagggtgaacctggaatt	1980
	caagggtgctggggcttctgggtcaagggagaaccaggagcaacgggttccccagga	2040
35	gaaccaggatacatgggtttaccgggattcaaggaaaaaagggggacaaaggaaatcaa	2100
	gggtgaaaaagggtattcaggggtcaaaaggagaaaaatggaagacagggaattccagggcaa	2160
	cagggaattcaaggccatcatgggtgcaaaaggagagagaggtgaaaagggagaaacctggt	2220
	gtccgaggtgccattggatcaaaaggagaatctgggtggatggcttgatggggcccgcga	2280
	ggtcctaaggggcaacctggggatccagggtcctcagggacccccagggttggatgggaag	2340
40	cccgaagagagttttcagaacaatttattcgacaagtttgacagatgtaataagagcc	2400
	cagctaccagtccttacttcagagtggagaatttagaaattgtgatcattgcctgtcccaa	2460

catggctccccgggtattcctggggccacctgggtccgataggcccagagggtcccagagga 2520
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gggtgtcagaggattaaaaggcctaccaggaagaaatggggaaaaagggagccaagggttt 2640
gggtatcctggagaacaaggtcctcctgggtccccaggtccagagggccctcctggaata 2700
5 agcaaagaaggtcctccaggagaccaggtctccctggcaaagatggagaccatggaaaa 2760
cctggaatccaagggcaaccaggccccccaggcacatctgcgacccatcactatgttttagt 2820
gtaattgccagaagagatccgttcagaaaaggaccaaactattag 2865

SEQ ID NO: 6

- 10 (ii) SEQUENCE CHARACTERISTICS:
(C) LENGTH: 22 bases
(D) TYPE: Nucleic acid
(vi) MOLECULE TYPE: oligonucleotide
(vii) FEATURE: artificial sequence

15

GGTTC ACCTT TGCTT CCCTT AG

SEQ ID NO: 7

- (iii) SEQUENCE CHARACTERISTICS:
20 (E) LENGTH: 23 bases
(F) TYPE: nucleic acid
(viii) MOLECULE TYPE: oligonucleotide
(ix) FEATURE: artificial sequence

25 TTGGC CCATT AATCC TCGGT TTC

SEQ ID NO: 8

- (iv) SEQUENCE CHARACTERISTICS:
(G) LENGTH: 24 bases
30 (H) TYPE: nucleic acid
(x) MOLECULE TYPE: oligonucleotide
(xi) FEATURE: artificial sequence

ATTCC TGGGC CACCT GGTCC GATA

SEQ ID NO: 9

(v) SEQUENCE CHARACTERISTICS:

(I) LENGTH: 21 bases

5 (J) TYPE: nucleic acid

(xii) MOLECULE TYPE: oligonucleotide

(xiii) FEATURE: artificial sequence

CTAAT AGTTT GGTCC TTTTC T

10

SEQ ID NO: 10

(vi) SEQUENCE CHARACTERISTICS:

(K) LENGTH: 26 bases

(L) TYPE: nucleic acid

15 (xiv) MOLECULE TYPE: oligonucleotide

(xv) FEATURE: artificial sequence

TGAAG GTCGG AGTCA ACGGA TTTGG T

20 SEQ ID NO: 11

(vii) SEQUENCE CHARACTERISTICS:

(M) LENGTH: 24 bases

(N) TYPE: nucleic acid

(xvi) MOLECULE TYPE: oligonucleotide

25 (xvii) FEATURE: artificial sequence

CATGT GGGCC ATGAG GTCCA CCAC

SEQ ID NO: 12

30 (viii) SEQUENCE CHARACTERISTICS:

(O) LENGTH: 23 bases

(P) TYPE: nucleic acid

(xviii) MOLECULE TYPE: oligonucleotide

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(xix)FEATURE: artificial sequence

TTCCT GGAAA CCGAG GATTA ATG

5 SEQ ID NO: 13

(ix) SEQUENCE CHARACTERISTICS:

(Q) LENGTH: 22 bases

(R) TYPE: nucleic acid

(xx) MOLECULE TYPE: oligonucleotide

10 (xxi)FEATURE: artificial sequence

AGTCC ACGAT CACCC TTGTC AC

SEQ ID NO: 14

15 (x) SEQUENCE CHARACTERISTICS:

(S) LENGTH: 24 bases

(T) TYPE: nucleic acid

(xxii) MOLECULE TYPE: oligonucleotide

(xxiii) FEATURE: artificial sequence

20

ATGGC TCACT ATATT ACATT TCTC

SEQ ID NO: 15

(xi) SEQUENCE CHARACTERISTICS:

25 (U) LENGTH: 43 bases

(V) TYPE: nucleic acid

(xxiv) MOLECULE TYPE: oligonucleotide

(xxv)FEATURE: artificial sequence

30 TTAGT GATGG TGATG GTGAT GCTCA TAGTT TGGTC CTTTT CTG